

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=1; day=6; hr=14; min=4; sec=17; ms=947;]

=====

Application No: 10539956 Version No: 3.0

Input Set:

Output Set:

Started: 2009-12-16 16:04:30.830
Finished: 2009-12-16 16:04:35.064
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 234 ms
Total Warnings: 16
Total Errors: 0
No. of SeqIDs Defined: 116
Actual SeqID Count: 116

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (98)
W 213	Artificial or Unknown found in <213> in SEQ ID (99)
W 213	Artificial or Unknown found in <213> in SEQ ID (100)
W 213	Artificial or Unknown found in <213> in SEQ ID (101)
W 213	Artificial or Unknown found in <213> in SEQ ID (102)
W 213	Artificial or Unknown found in <213> in SEQ ID (103)
W 213	Artificial or Unknown found in <213> in SEQ ID (104)
W 213	Artificial or Unknown found in <213> in SEQ ID (105)
W 213	Artificial or Unknown found in <213> in SEQ ID (107)

SEQUENCE LISTING

<110> NORRIS, STEVEN J.

<120> VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA SPECIES AND STRAINS

<130> UTSH:264US

<140> 10539956

<141> 2006-04-06

<150> PCT/US03/041182

<151> 2003-12-22

<150> 60/435,077

<151> 2002-12-20

<160> 116

<170> PatentIn Ver. 2.1

<210> 1

<211> 1227

<212> DNA

<213> *Borrelia burgdorferi*

<220>

<221> CDS

<222> (75)..(1142)

<400> 1

acctacactt gttaaaactc tctttttgag ttaagatgat aacttatact tttcattata 60

aggagacgat	gaat	atg	aaa	aaa	att	tca	agt	gca	agt	tta	tta	aca	act	110
	Met	Lys	Lys	Ile	Ser	Ser	Ala	Ser	Leu	Leu	Thr	Thr		
	1				5					10				

ttc	ttt	gtt	ttt	att	aat	tgt	aaa	agc	caa	gtt	gct	gat	aag	gac	gac	158
Phe	Phe	Val	Phe	Ile	Asn	Cys	Lys	Ser	Gln	Val	Ala	Asp	Lys	Asp	Asp	
	15					20					25					

cca	aca	aac	aaa	ttt	tac	caa	tct	gtc	ata	caa	tta	ggt	aac	gga	ttt	206
Pro	Thr	Asn	Lys	Phe	Tyr	Gln	Ser	Val	Ile	Gln	Leu	Gly	Asn	Gly	Phe	
	30					35					40					

ctt	gat	gta	ttc	aca	tct	ttt	ggg	ggg	tta	gta	gca	gag	gct	ttt	gga	254
Leu	Asp	Val	Phe	Thr	Ser	Phe	Gly	Gly	Leu	Val	Ala	Glu	Ala	Phe	Gly	
	45				50				55					60		

ttt	aaa	tca	gat	cca	aaa	aaa	tct	gat	gta	aaa	acc	tat	ttt	act	act	302
Phe	Lys	Ser	Asp	Pro	Lys	Lys	Ser	Asp	Val	Lys	Thr	Tyr	Phe	Thr	Thr	
				65					70					75		

gta	gct	gcc	aaa	ttg	gaa	aaa	aca	aaa	acc	gat	ctt	aat	agt	ttg	cct	350
Val	Ala	Ala	Lys	Leu	Glu	Lys	Thr	Lys	Thr	Asp	Leu	Asn	Ser	Leu	Pro	
			80					85						90		

aag gaa aaa agc gat ata agt agt acg acg ggg aaa cca gat agt aca	398
Lys Glu Lys Ser Asp Ile Ser Ser Thr Thr Gly Lys Pro Asp Ser Thr	
95 100 105	
ggg tct gtt gga act gcc gtt gag ggg gct att aag gaa gtt agc gag	446
Gly Ser Val Gly Thr Ala Val Glu Gly Ala Ile Lys Glu Val Ser Glu	
110 115 120	
ttg ttg gat aag ctg gta aaa gct gta aag aca gct gag ggg gct tca	494
Leu Leu Asp Lys Leu Val Lys Ala Val Lys Thr Ala Glu Gly Ala Ser	
125 130 135 140	
agt ggt act gct gca att gga gaa gtt gtg gct gat gct gat gct gca	542
Ser Gly Thr Ala Ala Ile Gly Glu Val Val Ala Asp Ala Asp Ala Ala	
145 150 155	
aag gtt gct gat aag gcg agt gtg aag ggg att gct aag ggg ata aag	590
Lys Val Ala Asp Lys Ala Ser Val Lys Gly Ile Ala Lys Gly Ile Lys	
160 165 170	
gag att gtt gaa gct gct ggg ggg agt gaa aag ctg aaa gct gtt gct	638
Glu Ile Val Glu Ala Ala Gly Gly Ser Glu Lys Leu Lys Ala Val Ala	
175 180 185	
gct gct aaa ggg gag aat aat aaa ggg gca ggg aag ttg ttt ggg aag	686
Ala Ala Lys Gly Glu Asn Asn Lys Gly Ala Gly Lys Leu Phe Gly Lys	
190 195 200	
gct ggt gct gct gct cat ggg gac agt gag gct gct agc aag gcg gct	734
Ala Gly Ala Ala Ala His Gly Asp Ser Glu Ala Ala Ser Lys Ala Ala	
205 210 215 220	
ggg gct gtt agt gct gtt agt ggg gag cag ata tta agt gcg att gtt	782
Gly Ala Val Ser Ala Val Ser Gly Glu Gln Ile Leu Ser Ala Ile Val	
225 230 235	
acg gct gct gat gcg gct gag cag gat gga aag aag cct gag gag gct	830
Thr Ala Ala Asp Ala Ala Glu Gln Asp Gly Lys Lys Pro Glu Glu Ala	
240 245 250	
aaa aat ccg att gct gct gct att ggg gat aaa gat ggg ggt gcg gag	878
Lys Asn Pro Ile Ala Ala Ala Ile Gly Asp Lys Asp Gly Gly Ala Glu	
255 260 265	
ttt ggt cag gat gag atg aag aag gat gat cag att gct gct gct att	926
Phe Gly Gln Asp Glu Met Lys Lys Asp Asp Gln Ile Ala Ala Ala Ile	
270 275 280	
gct ttg agg ggg atg gct aag gat gga aag ttt gct gtg aag gat ggt	974
Ala Leu Arg Gly Met Ala Lys Asp Gly Lys Phe Ala Val Lys Asp Gly	
285 290 295 300	
gag aaa gag aag gct gag ggg gct att aag gga gct gct gag tct gca	1022
Glu Lys Glu Lys Ala Glu Gly Ala Ile Lys Gly Ala Ala Glu Ser Ala	
305 310 315	

gtt cgc aaa gtt tta ggg gct att act ggg cta ata gga gac gcc gtg 1070
Val Arg Lys Val Leu Gly Ala Ile Thr Gly Leu Ile Gly Asp Ala Val
320 325 330

agt tcc ggg cta agg aaa gtc ggt gat tca gtg aag gct gct agt aaa 1118
Ser Ser Gly Leu Arg Lys Val Gly Asp Ser Val Lys Ala Ala Ser Lys
335 340 345

gaa aca cct cct gcc ttg aat aag tgatttaatt aagtgtatgg acacgactat 1172
Glu Thr Pro Pro Ala Leu Asn Lys
350 355

gccctcatga ttgaggaaat agtcgagaga tatatatact aaaagataat aaata 1227

<210> 2

<211> 356

<212> PRT

<213> Borrelia burgdorferi

<400> 2

Met Lys Lys Ile Ser Ser Ala Ser Leu Leu Thr Thr Phe Phe Val Phe
1 5 10 15

Ile Asn Cys Lys Ser Gln Val Ala Asp Lys Asp Asp Pro Thr Asn Lys
20 25 30

Phe Tyr Gln Ser Val Ile Gln Leu Gly Asn Gly Phe Leu Asp Val Phe
35 40 45

Thr Ser Phe Gly Gly Leu Val Ala Glu Ala Phe Gly Phe Lys Ser Asp
50 55 60

Pro Lys Lys Ser Asp Val Lys Thr Tyr Phe Thr Thr Val Ala Ala Lys
65 70 75 80

Leu Glu Lys Thr Lys Thr Asp Leu Asn Ser Leu Pro Lys Glu Lys Ser
85 90 95

Asp Ile Ser Ser Thr Thr Gly Lys Pro Asp Ser Thr Gly Ser Val Gly
100 105 110

Thr Ala Val Glu Gly Ala Ile Lys Glu Val Ser Glu Leu Leu Asp Lys
115 120 125

Leu Val Lys Ala Val Lys Thr Ala Glu Gly Ala Ser Ser Gly Thr Ala
130 135 140

Ala Ile Gly Glu Val Val Ala Asp Ala Asp Ala Ala Lys Val Ala Asp
145 150 155 160

Lys Ala Ser Val Lys Gly Ile Ala Lys Gly Ile Lys Glu Ile Val Glu
165 170 175

Ala Ala Gly Gly Ser Glu Lys Leu Lys Ala Val Ala Ala Ala Lys Gly
180 185 190

Glu Asn Asn Lys Gly Ala Gly Lys Leu Phe Gly Lys Ala Gly Ala Ala
 195 200 205
 Ala His Gly Asp Ser Glu Ala Ala Ser Lys Ala Ala Gly Ala Val Ser
 210 215 220
 Ala Val Ser Gly Glu Gln Ile Leu Ser Ala Ile Val Thr Ala Ala Asp
 225 230 235 240
 Ala Ala Glu Gln Asp Gly Lys Lys Pro Glu Glu Ala Lys Asn Pro Ile
 245 250 255
 Ala Ala Ala Ile Gly Asp Lys Asp Gly Gly Ala Glu Phe Gly Gln Asp
 260 265 270
 Glu Met Lys Lys Asp Asp Gln Ile Ala Ala Ala Ile Ala Leu Arg Gly
 275 280 285
 Met Ala Lys Asp Gly Lys Phe Ala Val Lys Asp Gly Glu Lys Glu Lys
 290 295 300
 Ala Glu Gly Ala Ile Lys Gly Ala Ala Glu Ser Ala Val Arg Lys Val
 305 310 315 320
 Leu Gly Ala Ile Thr Gly Leu Ile Gly Asp Ala Val Ser Ser Gly Leu
 325 330 335
 Arg Lys Val Gly Asp Ser Val Lys Ala Ala Ser Lys Glu Thr Pro Pro
 340 345 350
 Ala Leu Asn Lys
 355

<210> 3
 <211> 1141
 <212> DNA
 <213> *Borrelia hermsii*

<220>
 <221> CDS
 <222> (1)..(1062)

<400> 3
 atg aga aaa aga ata agt gca ata ata atg act tta ttt atg gta tta 48
 Met Arg Lys Arg Ile Ser Ala Ile Ile Met Thr Leu Phe Met Val Leu
 1 5 10 15
 gta agc tgt aat agc ggt ggg gtt gcg gaa gat cct aaa act gtg tat 96
 Val Ser Cys Asn Ser Gly Gly Val Ala Glu Asp Pro Lys Thr Val Tyr
 20 25 30
 tta aca tct ata gct aat tta ggg aaa gga ttt tta gat gtt ttt gtg 144
 Leu Thr Ser Ile Ala Asn Leu Gly Lys Gly Phe Leu Asp Val Phe Val
 35 40 45
 act ttt gga gat atg gtt act gga gct ttt ggt att aag gca gat act 192

Thr Phe Gly Asp Met Val Thr Gly Ala Phe Gly Ile Lys Ala Asp Thr	
50 55 60	
aag aaa agt gat ata ggg aag tat ttt act gat att gag agc act atg	240
Lys Lys Ser Asp Ile Gly Lys Tyr Phe Thr Asp Ile Glu Ser Thr Met	
65 70 75 80	
aca tca gtt aaa aag aag ttg caa gat gaa gtt gct aag aat ggt aac	288
Thr Ser Val Lys Lys Lys Leu Gln Asp Glu Val Ala Lys Asn Gly Asn	
85 90 95	
tat cca aag gta aag aca gct gtt gac gaa ttt gtt gca atc tta gga	336
Tyr Pro Lys Val Lys Thr Ala Val Asp Glu Phe Val Ala Ile Leu Gly	
100 105 110	
aag atc gag aaa gga gca aaa gaa gca tct aaa ggg gct act ggt gat	384
Lys Ile Glu Lys Gly Ala Lys Glu Ala Ser Lys Gly Ala Thr Gly Asp	
115 120 125	
gtt att att ggg aat act gtt aag aat ggt gat gct gta cct gga gaa	432
Val Ile Ile Gly Asn Thr Val Lys Asn Gly Asp Ala Val Pro Gly Glu	
130 135 140	
gca aca agt gtc aat tct ctt gtt aaa gga att aaa gaa ata gtt ggg	480
Ala Thr Ser Val Asn Ser Leu Val Lys Gly Ile Lys Glu Ile Val Gly	
145 150 155 160	
gta gtc ttg aag gaa ggt aag gca gat gct gat gct act aaa gat gat	528
Val Val Leu Lys Glu Gly Lys Ala Asp Ala Asp Ala Thr Lys Asp Asp	
165 170 175	
agt aag aaa gat att ggt aaa tta ttt acc gca acc act gat gcg aat	576
Ser Lys Lys Asp Ile Gly Lys Leu Phe Thr Ala Thr Thr Asp Ala Asn	
180 185 190	
aga gct gat aat gcg gca gct caa gca gct gca gcg tca ata gga gca	624
Arg Ala Asp Asn Ala Ala Ala Gln Ala Ala Ala Ala Ser Ile Gly Ala	
195 200 205	
gtg aca ggt gct gat atc ttg caa gct ata gta caa tct aag gaa aat	672
Val Thr Gly Ala Asp Ile Leu Gln Ala Ile Val Gln Ser Lys Glu Asn	
210 215 220	
cct gtt gca aat agt act gat gga att gaa aaa gca aca gat gca gct	720
Pro Val Ala Asn Ser Thr Asp Gly Ile Glu Lys Ala Thr Asp Ala Ala	
225 230 235 240	
gag att gca gtt gct cca gct aaa gat aat aaa aaa gag att aaa gat	768
Glu Ile Ala Val Ala Pro Ala Lys Asp Asn Lys Lys Glu Ile Lys Asp	
245 250 255	
gga gca aaa aaa gac gca gtt att gct gca ggc att gca ctg cga gca	816
Gly Ala Lys Lys Asp Ala Val Ile Ala Ala Gly Ile Ala Leu Arg Ala	
260 265 270	
atg gct aag aat ggt aca ttt tct att aaa aac aat gaa gat gcg gct	864
Met Ala Lys Asn Gly Thr Phe Ser Ile Lys Asn Asn Glu Asp Ala Ala	

275

280

285

gta acg acg ata aat agt gca gca gca agc gca gtg aac aag att tta 912
 Val Thr Thr Ile Asn Ser Ala Ala Ala Ser Ala Val Asn Lys Ile Leu
 290 295 300

agc act cta ata ata gca ata agg aat aca gtt gat agt ggt tta aaa 960
 Ser Thr Leu Ile Ile Ala Ile Arg Asn Thr Val Asp Ser Gly Leu Lys
 305 310 315 320

aca ata aat gag gct ctt gct aca gtt aaa caa gaa gat aaa tct gta 1008
 Thr Ile Asn Glu Ala Leu Ala Thr Val Lys Gln Glu Asp Lys Ser Val
 325 330 335

gaa gca act aat act gca gaa gca aca act agt ggt cag caa gcg aaa 1056
 Glu Ala Thr Asn Thr Ala Glu Ala Thr Thr Ser Gly Gln Gln Ala Lys
 340 345 350

aac tag ttaagggtaa atataaagga taaagttatt gtaagggaaa agcttttctt 1112
 Asn

gtttttaatg caggaatgta gtttctctg 1141

<210> 4

<211> 353

<212> PRT

<213> Borrelia hermsii

<400> 4

Met Arg Lys Arg Ile Ser Ala Ile Ile Met Thr Leu Phe Met Val Leu
 1 5 10 15
 Val Ser Cys Asn Ser Gly Gly Val Ala Glu Asp Pro Lys Thr Val Tyr
 20 25 30
 Leu Thr Ser Ile Ala Asn Leu Gly Lys Gly Phe Leu Asp Val Phe Val
 35 40 45
 Thr Phe Gly Asp Met Val Thr Gly Ala Phe Gly Ile Lys Ala Asp Thr
 50 55 60
 Lys Lys Ser Asp Ile Gly Lys Tyr Phe Thr Asp Ile Glu Ser Thr Met
 65 70 75 80
 Thr Ser Val Lys Lys Lys Leu Gln Asp Glu Val Ala Lys Asn Gly Asn
 85 90 95
 Tyr Pro Lys Val Lys Thr Ala Val Asp Glu Phe Val Ala Ile Leu Gly
 100 105 110
 Lys Ile Glu Lys Gly Ala Lys Glu Ala Ser Lys Gly Ala Thr Gly Asp
 115 120 125
 Val Ile Ile Gly Asn Thr Val Lys Asn Gly Asp Ala Val Pro Gly Glu
 130 135 140
 Ala Thr Ser Val Asn Ser Leu Val Lys Gly Ile Lys Glu Ile Val Gly
 145 150 155 160
 Val Val Leu Lys Glu Gly Lys Ala Asp Ala Asp Ala Thr Lys Asp Asp
 165 170 175
 Ser Lys Lys Asp Ile Gly Lys Leu Phe Thr Ala Thr Thr Asp Ala Asn
 180 185 190
 Arg Ala Asp Asn Ala Ala Ala Gln Ala Ala Ala Ala Ser Ile Gly Ala
 195 200 205
 Val Thr Gly Ala Asp Ile Leu Gln Ala Ile Val Gln Ser Lys Glu Asn

210	215	220
Pro Val Ala Asn Ser Thr Asp Gly Ile Glu Lys Ala Thr Asp Ala Ala		
225	230	235
Glu Ile Ala Val Ala Pro Ala Lys Asp Asn Lys Lys Glu Ile Lys Asp		240
245	250	255
Gly Ala Lys Lys Asp Ala Val Ile Ala Ala Gly Ile Ala Leu Arg Ala		
260	265	270
Met Ala Lys Asn Gly Thr Phe Ser Ile Lys Asn Asn Glu Asp Ala Ala		
275	280	285
Val Thr Thr Ile Asn Ser Ala Ala Ala Ser Ala Val Asn Lys Ile Leu		
290	295	300
Ser Thr Leu Ile Ile Ala Ile Arg Asn Thr Val Asp Ser Gly Leu Lys		
305	310	315
Thr Ile Asn Glu Ala Leu Ala Thr Val Lys Gln Glu Asp Lys Ser Val		
325	330	335
Glu Ala Thr Asn Thr Ala Glu Ala Thr Thr Ser Gly Gln Gln Ala Lys		
340	345	350
Asn		

<210> 5
 <211> 416
 <212> DNA
 <213> Borrelia afzelii

<220>
 <221> CDS
 <222> (1)..(414)

<400> 5	
aag ggg att gcg aag ggg ata aag ggg att gtt gcg gct gct ggg aag	48
Lys Gly Ile Ala Lys Gly Ile Lys Gly Ile Val Ala Ala Ala Gly Lys	
1 5 10 15	
gct ttt ggc aag gat ggt gat gcg ctg aca ggt gtt gca aaa gct gct	96
Ala Phe Gly Lys Asp Gly Asp Ala Leu Thr Gly Val Ala Lys Ala Ala	
20 25 30	
gag aat gat gct aac aag gat gcg ggg aag ttg ttt gct ggt aag aat	144
Glu Asn Asp Ala Asn Lys Asp Ala Gly Lys Leu Phe Ala Gly Lys Asn	
35 40 45	
ggt aat gct ggt gct gct gac att gcg aag gcg gct gct gct gtt act	192
Gly Asn Ala Gly Ala Ala Asp Ile Ala Lys Ala Ala Ala Ala Val Thr	
50 55 60	
gcg gtt agt ggg gag cag ata cta aaa gct att gtt gag gcg gct ggt	240
Ala Val Ser Gly Glu Gln Ile Leu Lys Ala Ile Val Glu Ala Ala Gly	
65 70 75 80	
gat gcg gat cag gcg ggt gta aag gct gat gcg gct aag aat ccg att	288
Asp Ala Asp Gln Ala Gly Val Lys Ala Asp Ala	